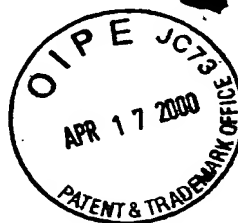


SEQUENCE LISTING



<110> Hope, Ernest G
Negrin, Robert

<120> COMPOSITIONS AND METHODS FOR PROTECTING ORGANS, TISSUE
AND CELLS FROM IMMUNE SYSTEM-MEDIATED DAMAGE

<130> A-67031-1/RFT

<140> 09/382,088

<141> 1999-08-24

<150> 60/097,640

<151> 1998-08-24

<160> 30

<170> PatentIn Ver. 2.1

<210> 1

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (1)

<223> X at position 1 can be V, L, A or T.

<220>

<221> SITE

<222> (2)

<223> X at position 2 can be L or H.

<220>

<221> SITE

<222> (3)

<223> X at position 3 can be S or V.

<220>

<221> SITE

<222> (4)

<223> X at position 4 can be D or E.

<220>

<221> SITE

<222> (5)

<223> X at position 5 can be Q,K or R.

<220>

<221> SITE

<222> (6)

<223> X at position 6 can be L or V.

<220>

<223> Description of Artificial Sequence: consensus
sequence.

<400> 1

Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg

1

5

<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (1)..(3)

<223> X at positions 1, 2, or 3 can be any amino acid.

<220>

<223> Description of Artificial Sequence: consensus
sequence.

<400> 2

Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg

1

5

<210> 3

<211> 9

<212> PRT

<213> Homo sapiens

<400> 3

Ala Val Leu Ser Ala Glu Gln Leu Arg

1

5

<210> 4

<211> 1254

<212> DNA

<213> Homo sapiens

<400> 4

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cgggttcctgt gtccgtcacc tctttagga ccacagtggg caccaccacc ggagcagcga 180
cccagagcac agcgaccgcg cgttcgctg gtgccgcagc gtccggttcc gtcacgactc 240
gcggtccttc acgcgagaga ggaagaccgc tgggaatacgg aggaccgaca cggggaccgt 300
gacgcgctgc tctccacgt gcggccggac ccactcgacg acgcgagtga gtcgttgagc 360
tgccgcgctg tgcactggac ctccgaccgc tcggtcgaca tgccctgggtc gagtcactcg 420
aagcgactac tgaagcacgc gtcgtcgttc gtcgtgatgt tgacgctcgt gaggttctag 480
ttgaagggcc tgcgcgctcg cgcgacgtca ggtagttgct caccgcggcg gtctggtggg 540
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caacggtaga ggaacgggtt cccacaccac ctccactggg tactggacgt ctttgtggac 960
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aagatgcggc tgggtgggaa gtagaaggac cagccctgtg gggtttcgcc gagggacgat 1200
aagtaaccgc cggaccaggc cgagttccca ctgttctacg ctctgctcaa tacc 1254
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<210> 5

<211> 1254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1251)

<400> 5

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Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
1 5 10 15

gca gcc gag gtg aag aaa cct gta gag gcc gca gcc cct ggt act gcg 96
Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
20 25 30

gag aag ctg agt tcc aag gcg acc aca ctg gca gag ccc agc aca ggc 144
Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
35 40 45
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ctg gcc ttc agc ctg tat cag gca atg gcc aag gac cag gca gtg gag	192
Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu	
50 55 60	
aac atc ctg gtg tca ccc gtg gtg gtg gcc tcg tcg ctg ggt ctc gtg	240
Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val	
65 70 75 80	
tcg ctg ggc ggc aag gcg acc acg gcg tcg cag gcc aag gca gtg ctg	288
Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu	
85 90 95	
agc gcc gag cag ctg cgc gac gag gag gtg cac gcc ggc ctg ggt gag	336
Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu	
100 105 110	
ctg ctg cgc tca ctc agc aac tcg acg gcg cgc aac gtg acc tgg aag	384
Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys	
115 120 125	
ctg ggc agc cga ctg tac gga ccc agc tca gtg agc ttc gct gat gac	432
Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp	
130 135 140	
ttc gtg gcg agc agc aag cag cac tac aac tgc gag cac tcc aag atc	480
Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile	
145 150 155 160	
aac ttc ccg gac aag cgc agc gcg ctg cag tcc atc aac gag tgg gcc	528
Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala	
165 170 175	
gcg cag acc acc gac ggc aag ctg ccc gag gtc acc aag gac gtg gag	576
Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu	
180 185 190	
agc acg gac ggc gcc ctg cta gtc aac gcc atg ttc ttc aag cca cac	624
Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His	
195 200 205	
tgg gat gag aaa ttc cac cac aag atg gtg gac aac cgt ggc ttc atg	672
Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met	
210 215 220	
gtg act cgg tcc tat act gtg ggt gtt acg atg atg cac cgg aca ggc	720
Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly	
225 230 235 240	

ctc tac aac tac tac gac gac gag aag gag aag ctg cag ctg gtg gag	768
Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu	
245 250 255	
atg ccc ctg gct cac aag ctc tcc agc ctc atc atc ctc atg ccc cat	816
Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His	
260 265 270	
cac gtg gag cct ctc gag cgc ctt gaa aag ctg cta acc aaa gag cag	864
His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln	
275 280 285	
ctg aag atc tgg atg ggg aag atg cag aag aag gct gtt gcc atc tcc	912
Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser	
290 295 300	
ttg ccc aag ggt gtg gtg gag gtg acc cat gac ctg cag aaa cac ctg	960
Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu	
305 310 315 320	
gct ggg ctg ggc ctg act gag gcc att gac aag aac aag gcc gac tta	1008
Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu	
325 330 335	
tca cgc atg tct ggc aag aag gat ctg tac ctg gcc agt gtg ttc cac	1056
Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His	
340 345 350	
gcc acc gcc ttt gag ttg gac aca gat ggc aac ccc ttt gac cag gac	1104
Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp	
355 360 365	
atc tac ggg cgc gag gag ctg cgc agc ccc aag ctg ttc tac gcc gac	1152
Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp	
370 375 380	
cac ccc ttc atc ttc ctg gtg cgg gac acc caa agc ggc tcc ctg cta	1200
His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu	
385 390 395 400	
ttc att ggg cgc ctg gtc cgg ctc aag ggt gac aag atg cga gac gag	1248
Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu	
405 410 415	
tta tag	1254
Leu	

<210> 6

<211> 417

<212> PRT

<213> Homo sapiens

<400> 6

Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
1 5 10 15

Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
20 25 30

Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
35 40 45

Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
50 55 60

Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
65 70 75 80

Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
85 90 95

Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
100 105 110

Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
115 120 125

Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
130 135 140

Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
145 150 155 160

Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
165 170 175

Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
180 185 190

Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
195 200 205

Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
210 215 220

Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly
225 230 235 240

Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
245 250 255

Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
260 265 270

His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
275 280 285

Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
290 295 300

Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
305 310 315 320

Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu
325 330 335

Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His
340 345 350

Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp
355 360 365

Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp
370 375 380

His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu
385 390 395 400

Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
405 410 415

Leu

<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 7

Ala Ala His Val Ala Glu Gln Leu Arg

1

5

<210> 8

<211> 9

<212> PRT

<213> Rat

<400> 8

Ala Val Leu Ser Ala Glu Lys Leu Arg

1

5

<210> 9

<211> 9

<212> PRT

<213> Chicken

<400> 9

Ala Val Leu Ser Ala Asp Lys Leu Asn

1

5

<210> 10

<211> 9

<212> PRT

<213> Homo sapiens

<400> 10

Ala Thr Leu Ser Ala Glu Arg Val Arg

1

5

<210> 11

<211> 9

<212> PRT

<213> Cat

<400> 11

Ala Thr Leu Ser Ala Glu Lys Val Arg

1

5

<210> 12

<211> 9

<212> PRT

<213> Cow

<400> 12

Ala Ile Leu Ser Ala Glu Lys Val Asn

1

5

<210> 13

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (6)

<223> X at position 5 can be D or E.

<220>

<221> SITE

<222> (7)

<223> X at position 7 can be K or Q.

<220>

<223> Description of Artificial Sequence: consensus
sequence.

Q
<400> 13

Ala Val Leu Ser Ala Xaa Xaa Leu Arg

1

5

<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (2)

<223> The X at position 2 can be V, L or T.

<220>

<221> SITE

<222> (7)

<223> The X at position 7 can be Q, K, or R.

<220>

<221> SITE

<222> (8)

<223> The X at position 8 can be L or V.

<220>

<223> Description of Artificial Sequence: consensus
sequence.

<400> 14

Ala Xaa Leu Ser Ala Glu Xaa Xaa Arg

1

5

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence.

<400> 15

acgtttggat ccaggtgaag a

21

<210> 16

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence.

<400> 16

taccggttcc tg

12

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence.

<400> 17

gcaatggcca aggaccaggc agtggag

27

<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence.

<400> 18

acgctctgct caatatacctt aagtcta

27

<210> 19

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 19

Lys Asp Glu Leu

1

<210> 20

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 20

Arg Asp Glu Leu

1

<210> 21

<211> 17

<212> PRT

<213> Homo sapiens

<400> 21

Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
1 5 10 15

Ala

<210> 22

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 22

Arg Val Glu Leu
1

<210> 23

<211> 21

<212> DNA

<213> Homo sapiens

<400> 23

acgttttgat ccaggtgaag a 21

<210> 24

<211> 12

<212> DNA

<213> Homo sapiens

<400> 24

taccggttcc tg 12

<210> 25

<211> 27

<212> DNA

<213> Homo sapiens

<400> 25

gcaatggcca aggaccaggc agtggag 27

<210> 26
<211> 27
<212> DNA
<213> Homo sapiens

<400> 26
atctgaattc ctataactcg tctcgca

27

<210> 27
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<212> DNA
<213> Homo sapiens

<400> 27
cggaattctg gccgaggtga agaaacc

27

<210> 28
<211> 27
<212> DNA
<213> Homo sapiens

<400> 28
agttcccact gttctacgac ctagggc

27

<210> 29
<211> 28
<212> DNA
<213> Homo sapiens

<400> 29
cggtatcca gatctgtgtc caactcaa

28

<210> 30
<211> 27
<212> DNA
<213> Homo sapiens

<400> 30
cgggatccag cacctcctcg tcgcgca

27